

17319A

GenCore version 5.1.4-p5 4578
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On protein - protein search, using sw model

Run on: April 8, 2003, 14:23:18 ; Search time 40 Seconds
 (without alignments)
 1815.540 Million cell updates/sec

Title: US-09-001-737-8
 Perfect score: 2653
 Sequence: I MAKEIKFSADARAAKMRGVDD.....TPAPAMPAGHDPGNMGGGG 545

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext: 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database :

1: A_Genesed_101002:*

2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980 DAT:*

3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982 DAT:*

4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983 DAT:*

5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984 DAT:*

6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985 DAT:*

7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985 DAT:*

8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987 DAT:*

9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988 DAT:*

10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990 DAT:*

11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991 DAT:*

12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992 DAT:*

13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993 DAT:*

14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993 DAT:*

15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994 DAT:*

16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995 DAT:*

17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997 DAT:*

18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998 DAT:*

19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999 DAT:*

20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999 DAT:*

21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000 DAT:*

22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001 DAT:*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002 DAT:*

Pred. No. 19 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS					
RESULT	1	XX	XX	XX	XX
AAY2304	AY2304 standard; Protein: 545 AA.				
ID					
AC	AAY2304;				
DT	22-SEP-1999 (first entry)				
DE	Streptococcus pyogenes heat shock protein (Hsp)60-2.				
XX	Heat shock protein; Hsp60-2; immune response; Immunological carrier; cancer control; tumour; sarcoma; cancer; gene therapy.				
OS	Streptococcus pyogenes.				
PN	W0935270-A1.				
PD	15-JUL-1999.				
XX					
PF	29-DEC-1998; 98WO-CA01203.				
PR	31-DEC-1997; 97US-0001737.				
PA	(STRE-) STRESGEN BIOTECHNOLOGIES CORP.				
XX					
PT	Mizzen L, Wisniewski J;				
XX	WPI:1999-43097-36.				
DR	N-PDB: AAX86155.				
XX					
PT	New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis.				
PT					

XX
PS
XX
Claim 11; FIG 4A-B; 176pp; English.

The present sequence represents a heat shock protein, designated Hsp60-2. The protein, its fragments, variants and fusion proteins, are used to elicit or enhance an immune response against *Streptococcus*, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and therapeutically in gene therapy vectors.

XX
SQ Sequence 545 AA:

Query Match	Score	DB	Length	Best Local Similarity	Pred.	Mismatches	Indels	Gaps
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%	DB 20;	545;	100.0%; Pred. No. 6.9e-164;				

OY 1 MAKEIKFSADARAAMYRGVDMPLADTVKVLGPKGRNVYLEKAFGSPLITNDGVTKEIE 60
Db 1 MAKEIKFSADARAAMYRGVDMPLADTVKVLGPKGRNVYLEKAFGSPLITNDGVTKEIE 60

OY 61 LEDHFENNGAKLVSEVASKNTDIAGSGTTATVLTQAVHEGKNTAGANPIGIRGIE 120
Db 61 LEDHFENNGAKLVSEVASKNTDIAGSGTTATVLTQAVHEGKNTAGANPIGIRGIE 120

OY 121 TATATAVEALKAIKOPVSCKEALQAVASSRSEKGYISEAMERVGNDGVTIESRG 180
Db 121 TATATAVEALKAIKOPVSCKEALQAVASSRSEKGYISEAMERVGNDGVTIESRG 180

OY 181 METELEVVEGMOPDRGYSQWYMTNEKVADEIENFILITDKVSNIQDILPVEVLK 240
Db 181 METELEVVEGMOPDRGYSQWYMTNEKVADEIENFILITDKVSNIQDILPVEVLK 240

OY 241 TRPILLIADDYDGALPVNKTKRTGTYVAVKPGCDRKAMEDAILGGVVIT 300
Db 241 TRPILLIADDYDGALPVNKTKRTGTYVAVKPGCDRKAMEDAILGGVVIT 300

OY 301 EDLGELKDATTMGLQAKITVDKSTIVGEGSSEANTANIAALKSOLETTSDFR 360
Db 301 EDLGELKDATTMGLQAKITVDKSTIVGEGSSEANTANIAALKSOLETTSDFR 360

OY 361 EKLOERLAKLAGGYAVKVGAPTEALKEMKRIEDBALNATRAVEEGIVAGGSTALTV 420
Db 361 EKLOERLAKLAGGYAVKVGAPTEALKEMKRIEDBALNATRAVEEGIVAGGSTALTV 420

OY 421 IEKVAALEGGDDATGRIVRLRPEYQQLNACQEGSVWIDKKNSPAGFGNARTG 480
Db 421 IEKVAALEGGDDATGRIVRLRPEYQQLNACQEGSVWIDKKNSPAGFGNARTG 480

OY 481 EWVOMIKIGIDPYKVTASALONASASYSLILTEVVKNPAPATPAPAMPAGMDGM 540
Db 481 EWVOMIKIGIDPYKVTASALONASASYSLILTEVVKNPAPATPAPAMPAGMDGM 540

OY 541 GGMOG 545
Db 541 GGMOG 545

XX
RESULT 2
ABP28529 ID ABP28529 standard; Protein: 545 AA.
XX AC ABP28529;
XX DT 02-JUL-2002 (first entry)
XX

DB Streptococcus polypeptide SEQ ID NO 6234.
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX OS Streptococcus pyogenes.
XX PN WO200234771-A2.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001; 2001WO-GB04789.
XX PR 27-OCT-2000; 2000GB-0026133.
PR 24-NOV-2000; 2000GB-002827.
PR 07-MAR-2001; 2001GB-0005640.
XX PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX PI Teiford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
PI Tettelin H;
XX DR WPI: 2002-352316/38.
DR N-PDB; ABN69160.
XX FS Claim 1; Page 3786; 4525pp; English.
XX The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus (GBS) (streptococcus agalactiae) or group A streptococcus/GAS (streptococcus pyogenes), comprising one of 543 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1) nucleic acids encoding (1), ABN604-AIN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*. Nucleic acids encoding (1) are used to detect *Streptococcus* in a biological sample. (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by *Streptococcus* that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying *Streptococcus* proteins.
XX SQ Sequence 545 AA:
Query Match 99.2%; Score 2643; DB 23; Length 545:
Best Local Similarity 99.8%; Pred. No. 1.e-162;
Matches 541; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAKEIKFSADARAAMYRGVDMPLADTVKVLGPKGRNVYLEKAFGSPLITNDGVTKEIE 60
Db 3 MAKDIFKSADARAAMYRGVDMPLADTVKVLGPKGRNVYLEKAFGSPLITNDGVTKEIE 62

OY 61 LEDHFENNGAKLVSEVASKNTDIAGSGTTATVLTQAVHEGKNTAGANPIGIRGIE 120
Db 63 LEDHFENNGAKLVSEVASKNTDIAGSGTTATVLTQAVHEGKNTAGANPIGIRGIE 122

OY 121 TATATAVEALKAIKOPVSCKEALQAVASSRSEKGYISEAMERVGNDGVTIESRG 180
Db 123 TATATAVEALKAIKOPVSCKEALQAVASSRSEKGYISEAMERVGNDGVTIESRG 182

OY 181 METELEVVEGMOPDRGYSQWYMTNEKVADEIENFILITDKVSNIQDILPVEVLK 240
Db 183 METELEVVEGMOPDRGYSQWYMTNEKVADEIENFILITDKVSNIQDILPVEVLK 242

CC Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (II). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 Streptococcus that is prevented or treated may be meningitis. Nucleic
 acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

QY 241 TNRPLLIADDVGEALPFLVNLKIRGTFNMYAVRAGFGRKAMLEDAITLGCVIT 300
 Db 243 TNRPLLIADDVGEALPFLVNLKIRGTFNMYAVRAGFGRKAMLEDAITLGCVIT 302

QY 301 EDLGIELKADMTAGQAKTIVDKSFTVIEGSSEANANIALIKSOLETTSFDR 360
 Db 303 EDLGIELKADMTAGQAKTIVDKSFTVIEGSSEANANIALIKSOLETTSFDR 362

QY 361 EKQERLAKLAGGVAVIKVGAPEPTALKEMKRIEDALANATRAVERGTVAGGTALITY 420
 Db 363 EKQERLAKLAGGVAVIKVGAPEPTALKEMKRIEDALANATRAVERGTVAGGTALITY 422

QY 421 IEKVALELEGDDATGRNIYVRALEPVRQALNAGIESVVDLKNSPAGFNAATG 480
 Db 423 IEKVALELEGDDATGRNIYVRALEPVRQALNAGIESVVDLKNSPAGFNAATG 482

QY 481 EWMVKIGIIDPVYVTSLONAASVSLITTEAVANKPEPATPAPAMPGMGMM 540
 Db 483 EWMVKIGIIDPVYVTSLONAASVSLITTEAVANKPEPATPAPAMPGMGMM 542

QY 541 GG 542

Db 543 GG 544

RESULT 3

ABP28528 ABP28528 standard; Protein; 540 AA.
 XX AC ABP28528;
 XX DT 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 6232.
 XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX OS Streptococcus agalactiae.
 XX PN WO200234771-A2.
 XX PD 02-MAY-2002.
 XX PP 29-OCT-2001; 2001WO-GB04789.
 XX PR 27-OCT-2000; 2000GB-0026333.
 XX PR 24-NOV-2000; 2000GB-002727.
 XX PR 07-MAR-2001; 2001GB-0005640.

(CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX PI Telford J, Masiognani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX DR N-PSPB; ABN69159.
 XX PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX PS Claim 1, Page 3785, 4525pp, English.

RESULT 4

XX ID AAY23902
 XX PT AAY23902 standard; Protein; 541 AA.
 AC AAY23902;
 XX DT 22-SEP-1999 (first entry)
 XX DE Streptococcus pneumoniae heat shock protein (Hsp)60-2.
 XX KW Heat shock protein; Hsp60-2; immune response; immunological carrier;
 KW cancer control; tumour; sarcoma; cancer; gene therapy.
 OS Streptococcus pneumoniae.

The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 543 sequences (S1), given in the specification. The proteins have antibacterial and anti-inflammatory activity. (I), nucleic acids encoding (I), ABN69159, ABN6044, ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by

PN	WO935370-A1.
XX	PD 15-JUL-1999.
XX	PT 29-DEC-1998; 98W0-CA01203.
XX	PR 31-DEC-1997; 97US-0001737.
XX	PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX	PI Mizzen L, Wisniewski J;
XX	DR WPI: 1999-430397/36;
XX	N-PSDB: AAX86153.
XX	PT New nucleic acid encoding heat shock protein-60 from <i>Streptococcus</i> , useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis.
XX	PR Claim 11; FIG 2A-B; 176pp; English.
XX	The present sequence represents a heat shock protein, designated Hsp60-2. The protein, its fragments, variants and fusion proteins, are used to elicit or enhance an immune response against <i>Streptococcus</i> , and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting <i>Streptococci</i> in standard hybridization, amplification assays, and therapeutically in gene therapy vectors.
SQ Sequence 541 AA;	
Query Match 88.5%; Score 2358; DB 20; Length 541; Best Local Similarity 87.9%; Pred. No. 3.1e-14; Matches 479; Conservative 33; Mismatches 29; Indels 4; Gaps 1;	
OY 1 MAKEIKFSADARMYRGUDMLADTVKVLGPKGRNVLEKAFGSPPLITNGVIAKE 60	
Db 1 MAKEIKFSSDARSAMYRGUDMLADTVKVLGPKGRNVLEKAFGSPPLITNGVIAKE 60	
OY 61 LEDHENMKAJLVSEVAKNDIAGDGTTATVQIIVHGLNYAGAPIGIRGIE 120	
Db 61 LEDDHFMKGAKLVAEVASKNDIAGDGTTATVQIIVHGLNYAGAPIGIRGIE 120	
OY 121 TATAATVAKLAQPVSGTEAAQAVAVSVRSKVEYSEANERYGVNDVTEESRG 180	
Db 121 TATAATVAKLAQPVSGTEAAQAVAVSVRSKVEYSEANERYGVNDVTEESRG 180	
OY 181 METELEVVGGMDRQGYLSQWYMTNEKMYADLNPLNPTLDDKKVSNQDILPYLEVK 240	
Db 181 METELEVVGGMDRQGYLSQWYMTNEKMYADLNPLNPTLDDKKVSNQDILPYLEVK 240	
OY 241 TWRPLLIADDVGAEALPVLVNUKIRGTFENVAKARGFGDRRKAMLDIAITGGVIT 300	
Db 241 TWRPLLIADDVGAEALPVLVNUKIRGTFENVAKARGFGDRRKAMLDIAITGGVIT 300	
SQ Sequence 641 AA;	
Query Match 88.5%; Score 2358; DB 22; Length 641; Best Local Similarity 87.9%; Pred. No. 4.1e-14; Matches 479; Conservative 33; Mismatches 29; Indels 4; Gaps 1;	
OY 1 MAKEIKFSADARMYRGUDMLADTVKVLGPKGRNVLEKAFGSPPLITNGVIAKE 60	
Db 1 MAKEIKFSSDARSAMYRGUDMLADTVKVLGPKGRNVLEKAFGSPPLITNGVIAKE 60	
OY 61 LEDHENMKAJLVSEVAKNDIAGDGTTATVQIIVHGLNYAGAPIGIRGIE 120	

RESULT 6

Db 61 LEDHRENNGAKLVSEVASKTNDIAGDGTTATVLTOAVREGIKNTAGANPPIGIRGIE 120
 Qy 121 TATTAVALKAQIAQPSKGKAIQAOYAVSSRSERKEVISEAMERYGNQVITIERSRG 180
 Db 121 TATAAVALKAQIAQPSKGKAIQAOYAVSSRSERKEVISEAMERYGNQVITIERSRG 180
 Qy 181 METELEVVEGMOFDGYLSQMYTDNEKADLENPFILDKVSYQDILPLEVK 240
 Db 181 METELEVVEGMOFDGYLSQMYTDNEKADLENPFILDKVSYQDILPLEVK 240
 Qy 241 TNRPLIADDVDAQDGAQALPTVLINKTRGFTENYVAKPGFDRKAMLEDAILGGVIT 300
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 241 SNRPLIADDVDAQDGAQALPTVLINKTRGFTENYVAKPGFDRKAMLEDAILGGVIT 300
 Qy 301 EDIGLELKDATMAGQAQAKTVDKSDTVTVEGSSSEANRITALIKSQQETTSDFDR 360
 Db 301 EDIGLELKDATMAGQAQAKTVDKSDTVTVEGSSSEANRITALIKSQQETTSDFDR 360
 Qy 361 EKLOERLAKLKGSGVAVIKGAAVTELEKMKLRIEDALNATHRAVEEGIVAGGGTALANV 420
 Db 361 EKLOERLAKLKGSGVAVIKGAAVTELEKMKLRIEDALNATHRAVEEGIVAGGGTALANV 420
 Qy 421 IEKVALELEGDDTGINTIVRALEEPVQDQLNAGYEGSVWIDKLKNSPAGTGFNATG 480
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 421 IPAVATELDTGDEATGRNTIVRALEEPVQDQLNAGFEGSTIVIDRLKNELGIFNATG 480
 Qy 481 EWMWIKGIDPVPVTRSLONAASVSLILTEAWANKKEPATPAPAMPQMPGM 540
 Db 481 EWMWIKGIDPVPVTRSLONAASVSLILTEAWANKKEPATPAPAMPQMPGM 540
 Qy 541 GGCG 545
 Db 537 GGCG 541

RESULT 6

Db AAM01101 standard; Protein: 540 AA.
 AC AAM01101;
 DT 02-OCT-2001 (first entry)
 DE CFE 104 protein sequence.
 XX Antibacterial; vaccine; gene therapy; bacterial cell wall viability; CFE; CGC; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance.
 OS Streptococcus pneumoniae.
 PN WO200149721-A2.
 PD 12-JUL-2001.
 PF 29-DEC-2000; 200000-0535604.
 PR 30-DEC-1999; 99US-0174089.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA XX
 PI Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Brucoleri RE; Thunassi JB;
 XX DR
 DR N-PSDB; AAH90800.
 PT Nucleic acids encoding conserved essential genes involved in bacterial replication which are potential targets for the treatment of antibiotic resistant bacterial infections -
 PS Claim 27; Pages 356-358; 380pp; English.

Query Match 88.1%; Score 2347; DB 22; Length 540;
 Best Local Similarity 87.8%; Pred. No. 1.7e-143;
 Matches 47; Conservative 34; Mismatches 28; Indels 4; Gaps 1;

Db 1 MSKETKFSDARSAMVGYDILADTYKTVLPGKRNVLKSCSPNTDNGVIAKE 60
 Qy 61 LEDHRENNGAKLVSEVASKTNDIAGDGTTATVLTOAVREGIKNTAGANPPIGIRGIE 120
 Db 61 LEDHRENNGAKLVSEVASKTNDIAGDGTTATVLTOAVREGIKNTAGANPPIGIRGIE 120
 Qy 121 TATTAVALKAQIAQPSKGKAIQAOYAVSSRSERKEVISEAMERYGNQVITIERSRG 180
 Db 121 TATAAVALKAQIAQPSKGKAIQAOYAVSSRSERKEVISEAMERYGNQVITIERSRG 180
 Qy 181 METELEVVEGMOFDGYLSQMYTDNEKADLENPFILDKVSYQDILPLEVK 240
 Db 181 METELEVVEGMOFDGYLSQMYTDNEKADLENPFILDKVSYQDILPLEVK 240
 Qy 241 TNRPLIADDVDAQDGAQALPTVLINKTRGFTENYVAKPGFDRKAMLEDAILGGVIT 300
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 241 SNRPLIADDVDAQDGAQALPTVLINKTRGFTENYVAKPGFDRKAMLEDAILGGVIT 300
 Qy 301 EDIGLELKDATMAGQAQAKTVDKSDTVTVEGSSSEANRITALIKSQQETTSDFDR 360
 Db 301 EDIGLELKDATMAGQAQAKTVDKSDTVTVEGSSSEANRITALIKSQQETTSDFDR 360
 Qy 361 EKLOERLAKLKGSGVAVIKGAAVTELEKMKLRIEDALNATHRAVEEGIVAGGGTALANV 420
 Db 361 EKLOERLAKLKGSGVAVIKGAAVTELEKMKLRIEDALNATHRAVEEGIVAGGGTALANV 420
 Qy 421 IEKVALELEGDDTGINTIVRALEEPVQDQLNAGYEGSVWIDKLKNSPAGTGFNATG 480
 |||||:|||||:|||||:|||||:|||||:
 Db 421 IPAVATELDTGDEATGRNTIVRALEEPVQDQLNAGFEGSTIVIDRLKNELGIFNATG 480
 Qy 481 EWMWIKGIDPVPVTRSLONAASVSLILTEAWANKKEPATPAPAMPQMPGM 540
 Db 481 EWMWIKGIDPVPVTRSLONAASVSLILTEAWANKKEPATPAPAMPQMPGM 540
 Qy 541 GGCG 543
 Db 537 GGM 539

The present invention relates to nucleic acids (AAM00701-AAH90918) encoding polypeptides (AAM0002-AAM0114), which are essential for the viability of a bacterial cell wall. The acronym CFE stands for "CFE for Expression", where CEG stands for "Conserved Essential Gene". The nucleic acids are useful for detecting the presence of proteins essential for the viability of a bacterial cell wall in samples such as cells, tissues, biological fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleotide sequence of interest is essential for viability of a bacterial cell or whether it resides within an operon, by integrating an exogenous nucleotide sequence comprising a portion of an open reading frame of the genomic sequence of interest (comprising 200-500 base pairs) into the genomic sequence of interest which confers a selectable phenotype to the cell, and determining cell viability with a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and anti-sense therapy. The nucleic acids also enable identification of targets suitable for the treatment of antibiotic resistant bacterial infections.

Sequence 540 AA:

Query Match 88.1%; Score 2347; DB 22; Length 540;
 Best Local Similarity 87.8%; Pred. No. 1.7e-143;
 Matches 47; Conservative 34; Mismatches 28; Indels 4; Gaps 1;

Db 1 MSKETKFSDARSAMVGYDILADTYKTVLPGKRNVLKSCSPNTDNGVIAKE 60
 Qy 61 LEDHRENNGAKLVSEVASKTNDIAGDGTTATVLTOAVREGIKNTAGANPPIGIRGIE 120
 Db 61 LEDHRENNGAKLVSEVASKTNDIAGDGTTATVLTOAVREGIKNTAGANPPIGIRGIE 120
 Qy 121 TATTAVALKAQIAQPSKGKAIQAOYAVSSRSERKEVISEAMERYGNQVITIERSRG 180
 Db 121 TATAAVALKAQIAQPSKGKAIQAOYAVSSRSERKEVISEAMERYGNQVITIERSRG 180
 Qy 181 METELEVVEGMOFDGYLSQMYTDNEKADLENPFILDKVSYQDILPLEVK 240
 Db 181 METELEVVEGMOFDGYLSQMYTDNEKADLENPFILDKVSYQDILPLEVK 240
 Qy 241 TNRPLIADDVDAQDGAQALPTVLINKTRGFTENYVAKPGFDRKAMLEDAILGGVIT 300
 :|||||:|||||:|||||:|||||:|||||:|||||:
 Db 241 SNRPLIADDVDAQDGAQALPTVLINKTRGFTENYVAKPGFDRKAMLEDAILGGVIT 300
 Qy 301 EDIGLELKDATMAGQAQAKTVDKSDTVTVEGSSSEANRITALIKSQQETTSDFDR 360
 Db 301 EDIGLELKDATMAGQAQAKTVDKSDTVTVEGSSSEANRITALIKSQQETTSDFDR 360
 Qy 361 EKLOERLAKLKGSGVAVIKGAAVTELEKMKLRIEDALNATHRAVEEGIVAGGGTALANV 420
 Db 361 EKLOERLAKLKGSGVAVIKGAAVTELEKMKLRIEDALNATHRAVEEGIVAGGGTALANV 420
 Qy 421 IEKVALELEGDDTGINTIVRALEEPVQDQLNAGYEGSVWIDKLKNSPAGTGFNATG 480
 |||||:|||||:
 Db 421 IPAVATELDTGDEATGRNTIVRALEEPVQDQLNAGFEGSTIVIDRLKNELGIFNATG 480
 Qy 481 EWMWIKGIDPVPVTRSLONAASVSLILTEAWANKKEPATPAPAMPQMPGM 540
 Db 481 EWMWIKGIDPVPVTRSLONAASVSLILTEAWANKKEPATPAPAMPQMPGM 540
 Qy 541 GGCG 543
 Db 537 GGM 539

RESULT 7

Db ABB53701 standard; Protein: 542 AA.
 AC ABB53701;

CC	at ftp.wipo.int/pub/published_pct_sequences.	XX	XX
XX		PI	Mizzen L, Wisniewski J;
Sequence	542 AA;	XX	WI; 1999-430397/36.
Query Match	76.4%; Score 2033.5; DB 23; Length 542;	PT	New nucleic acid encoding heat shock protein-60 from Streptococcus,
Best Local Similarity 75.6%; Pred. No. 2.9e-123; Matches 412; Conservative 61; Mismatches 67; Indels 5; Gaps 3;	PT	useful in vaccines, as carriers for other immunogens, as anticancer	
Qy	1 MAKIKFSDARAAMRGYVDMPLADTVKTYLGPKGRNVLEKAFGSPLITNDGYTIKEIE 60	PT	agents and for diagnosis
Db	1 MAKIKFSDARAAMRGYVDMPLADTVKTYLGPKGRNVLEKAFGSPLITNDGYTIKEIE 60	XX	Disclosure; FIG 10A-E; 17pp; English.
Qy	61 LEDHFHENMGAKLYSEVAKNDTAGDTTAVLTLQAVHESCLKANTAGANPIGIRGIE 120	CC	AY23905.30 represent heat shock proteins (Hsps). The specification
Db	61 LEDPFENMGAKLYSEVAKNDTAGDTTAVLQAQMIQSGLKNTAGANPIGIRGIE 120	CC	describes Streptococcal Hsps, designated Hsp60. These proteins, their
Qy	121 TATAAAVEALKAJAQPVSGEATQAVAVASSEKRSERKVGYTSEAMERVENDGIVTEESG 180	CC	fragments, variants and fusion proteins, are used to elicit or enhance
Db	121 KAVATRIEELKAISKIESRESTKQVAISGDSDEVGKLAEAMERVGNDGYTIEBKG 180	CC	an immune response against Streptococcus, and to elicit a similar
Qy	181 METELEVGVGMGDFROYLSQMYTDNEKMDAQNPELITDVKYNSNQDILPYLEBEVK 240	CC	response to a target antigen fused to the protein. Unlike other
Db	181 FATELDVYEGMDFRPTSYMSYMTSDKMBRVLKPKYLIDKKINNOELPYLEQVHQ 240	CC	immunological carriers, Hsp60 proteins are not immunosuppressive so
Qy	241 TNRPPLIADDVGEALPTVNLKIRTFENVAVKAPGGRKAMLDIAILTGTWIT 300	CC	provide an increased response to any conjugated or fused antigen. Also,
Db	241 QGPMLILADEYEGEAOATVNLKLGTEFENVAVKAPGGRKAMLDIAILTGTWIT 300	CC	with endotoxins. They can also be used to detect specific antibodies
Qy	301 EDLGELKDMMTGQAKTVDKSTVVEGSSSEAIARIALIKSOLETTSDFR 360	CC	and in treatment or prevention of tumours (e.g. sarcoma or cancers of
Db	301 EDLGELKDMMTGQAKTVDKSTVVEGSSSEAIARIALIKSOLETTSDFR 360	CC	breast, ovary, prostate, lung, pancreas or liver). The Hsp60
Qy	361 EKIQERLAKLAGGVNVKVGAPTEAKMKRLDAEALNATRAAVEGIVAGGGTALIV 420	CC	polynucleotide is used for recombinant production of the protein, as
Db	361 EKIQERLAKLAGGVNVKVGAPTEAKMKRLDAEALNATRAAVEGIVAGGGTALIV 420	CC	a source of primers and probes for detecting streptococci in standard
Qy	421 IEKVALELEGDDATGRTNVLRLSERVORLNAALNAGYEGSVVQIKLUSPGTGAATG 480	CC	hybridization/amplification assays, and therapeutically in gene
Db	421 YNKVAALEREGOEVGINTVLSLEEFVROLAHAGLEGSVIVVERLKEHEAVGVFGNAANG 480	CC	therapy vectors.
Qy	4811 EWMDIKIGIIPDPVKTRALQNAASVASYLITTEAVVANKPEPATPAPMPGDPGM 540	XX	Sequence 544 AA;
Db	4811 EWMDIKIGIIPDPVKTRALQNAASVASYLITTEAVVANKPEPATPAPMPGDPGM 540	XX	Query Match 75.1%; Score 2026.5; DB 20; Length 544;
Qy	541 GGCG 545	PT	Best Local Similarity 75.8%; Pred. No. 8.3e-123; Matches 40; Conservative 69; Mismatches 71; Indels 3; Gaps 1;
Db	536 GGCG 540	XX	Matches 40; Conservative 69; Mismatches 71; Indels 3; Gaps 1;
RESULT 9		Qy	1 MAKIKFSDARAAMRGYVDMPLADTVKTYLGPKGRNVLEKAFGSPLITNDGYTIKEIE 60
ID AAY23905	AAY23905 standard; Protein: 544 AA.	Db	1 MAKIKFSDARAAMRGYVDMPLADTVKTYLGPKGRNVLEKAFGSPLITNDGYTIKEIE 60
AC AAY23905;		Qy	61 LEDPFENMGAKLYSEVAKNDTAGDTTAVLQAQMIQSGLKNTAGANPIGIRGIE 120
XX		Db	61 LEDPFENMGAKLYSEVAKNDTAGDTTAVLQAQMIQSGLKNTAGANPIGIRGIE 120
DT 22-SEP-1999 (first entry)		Qy	121 TATAAAVEALKAJAQPVSGEATQAVAVASSEKRSERKVGYTSEAMERVENDGIVTEESG 180
XX		Db	121 TATAAAVEALKAJAQPVSGEATQAVAVASSEKRSERKVGYTSEAMERVENDGIVTEESG 180
DE Amino acid sequence of a heat shock protein.		Qy	181 METELEVGVGMGDFRPTSYMSYMTSDKMBRVLKPKYLIDKKINNOELPYLEQVHQ 240
XX		Db	181 FTELEVGVGMGDFRPTSYMSYMTSDKMBRVLKPKYLIDKKINNOELPYLEQVHQ 240
XX		Qy	241 TNRPPLIADDVGEALPTVNLKIRTFENVAVKAPGGRKAMLDIAILTGTWIT 300
XX		Db	241 QGPMLILADEYEGEAOATVNLKLGTEFENVAVKAPGGRKAMLDIAILTGTWIT 300
XX		Qy	301 EDLGELKDMMTGQAKTVDKSTVVEGSSSEAIARIALIKSOLETTSDFR 360
XX		Db	301 EDLGELKDMMTGQAKTVDKSTVVEGSSSEAIARIALIKSOLETTSDFR 360
XX		Qy	361 EKIQERLAKLAGGVNVKVGAPTEAKMKRLDAEALNATRAAVEGIVAGGGTALIV 420
XX		Db	361 EKIQERLAKLAGGVNVKVGAPTEAKMKRLDAEALNATRAAVEGIVAGGGTALIV 420
XX		Qy	421 IEKVALELEGDDATGRTNVLRLSERVORLNAALNAGYEGSVVQIKLUSPGTGAATG 480
OS Bacillus subtilis.		Db	421 IEKVALELEGDDATGRTNVLRLSERVORLNAALNAGYEGSVVQIKLUSPGTGAATG 480
XX		Qy	4811 EWMDIKIGIIPDPVKTRALQNAASVASYLITTEAVVANKPEPATPAPMPGDPGM 540
PN W9935270-A1.		Db	4811 EWMDIKIGIIPDPVKTRALQNAASVASYLITTEAVVANKPEPATPAPMPGDPGM 540
XX		Qy	541 GGCG 545
PD 15-JUL-1999.		Db	538 GGCG 542
XX			{ STRE- } STRESSEN BIOTECHNOLOGIES CORP.

CC Polynucleotide sequences from the present invention, AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4456, so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 XX no sequences are present for SEQ ID NO:4455 to 4464.

SQ Sequence 539 AA;

Query Match 70.6%; Score 1880.5; DB 22; Length 539;
 Best Local Similarity 68.1%; Pred. No. 2.2e-113; PS
 Matches 368; Conservative 85; Mismatches 86; Indels 1; Gaps 1;

Oy 1 MAKEIKPSADARAAMVGYGMLADPKVYKLGKGRNVLEKARGSPPLITDGVTAKETE 60
 Db 1 MANDUKFESDAROMLRLRVDKLANAVKTVGPKGRNVVLDKDTPLITDGVTAKETE 60
 Oy 61 LEDHENMKAKLYSEVASKTDINDGTTTAVLQATWELKNTAGANPPIGIRGIE 120
 Db 61 LEDPYENNGAKLYVEVANKNEIAGDGTTTAVLAQSMIQEGLNVTSGANPVGLRGID 120
 Oy 121 TATATAVELAKIAQPYSGKAIQAVVASSERKEGETISAMERYNGDNGVTIBSRG 180
 Db 121 KAVOVIALEHESOKYENKEIAQVOGIAADEIGRIVISAMDRKGNGVTIBSRG 180
 Oy 181 MEVELEVNGMOPDRGLSLSQMTDNEMPLKLTOKVSNIDDLDELFVLR 240
 Db 181 FNTTELEVNGMOPDRGQYQSPYMWTSKMIABLERPYLVTDKTSFODILPLBQYO 240

SQ Sequence 539 AA;

Query Match 69.4%; Score 1847.5; DB 20; Length 539;
 Best Local Similarity 68.3%; Pred. No. 2.9e-111; PS
 Matches 371; Conservative 78; Mismatches 87; Indels 7; Gaps 4;

Oy 301 EDIGLGEKDTATMPALGQAKITVKDKSTVYEGGSSEATANRALIKSOLETTSDFR 360
 Db 301 DQGSLKIKDASDMLGTRKVKVETKDTWVGDNGDENNDARVGQKIAQIEPDSEFR 360
 Oy 361 EKIQERLAKLAGWAVKVKAPTEALKEMKLRTEDALNATRAVEEGTVAGSGTALIV 420
 Db 361 EKIQERLAKLAGWAVKVKAGASETELKERKLRIEDALNSTRAVEEGTVAGGTLVNI 420
 Oy 421 IEKVAALELEGDDATGNTTILRALEPYRQALNAGYEGSVMDKIKNSPAGTGFNATG 480
 Db 421 YOKVSEIKAEQDVETGVNLYNLQKAPVQPAENAGLSIVVERLIKHAEGYGFNATN 480
 Oy 481 ENWDMKTSITDVKYRSALQNAVASLILTEAVVANKKEPATPAPAMPMDPGMM 540
 Db 481 ENWNMLEEGIVDPKVTRSLQHASYAAMFLTEAVVASIPENNEOPOGMG-GMM 539

SQ Sequence 539 AA;

Query Match 69.4%; Score 1847.5; DB 20; Length 539;
 Best Local Similarity 68.3%; Pred. No. 2.9e-111; PS
 Matches 371; Conservative 78; Mismatches 87; Indels 7; Gaps 4;

Oy 1 MAKEIKPSADARAAMVGYGMLADPKVYKLGKGRNVLEKARGSPPLITDGVTAKETE 60
 Db 1 MANDUKFESDAROMLRLRVDKLANAVKTVGPKGRNVVLDKDTPLITDGVTAKETE 60
 Oy 61 LEDHENMKAKLYSEVASKTDINDGTTTAVLQATWELKNTAGANPPIGIRGIE 120
 Db 61 LEDPYENNGAKLYVEVANKNEIAGDGTTTAVLAQSMIQEGLNVTSGANPVGLRGID 120

SQ Sequence 539 AA;

Query Match 69.4%; Score 1847.5; DB 20; Length 539;
 Best Local Similarity 68.3%; Pred. No. 2.9e-111; PS
 Matches 371; Conservative 78; Mismatches 87; Indels 7; Gaps 4;

Oy 178 SRGMTELEWVNGMOPDRGLSLSQMTDNEMPLKLTOKVSNIDDLDELFVLR 237
 Db 181 SNRTEEL - GMOPDRQYQSPYMWTSKMIABLERPYLVTDKTSFODILPLBQ 238
 Oy 238 VLKTNPLLIADDVGEALPVLKIRGFTNNVAKAGFGSRKMLDTAIFTG 297
 Db 239 VVOSNRPLIVADEVEGDLNTVNRMRCTFAVAKAGFCGCRKAMLEDALITGAQ 298

SQ Sequence 539 AA;

Query Match 69.4%; Score 1847.5; DB 20; Length 539;
 Best Local Similarity 68.3%; Pred. No. 2.9e-111; PS
 Matches 371; Conservative 78; Mismatches 87; Indels 7; Gaps 4;

RESULT 12

AY23916 AAAY23916 standard; Protein; 539 AA.

XX AAV23916;

XX 22-SEP-1999 (first entry)

DE Amino acid sequence of a heat shock protein.

KW Heat shock protein; Hsp; immune response; immunological carrier; cancer control; tumour; sarcoma; cancer; gene therapy.

XX OS Staphylococcus aureus.

XX W0935370-A1.

XX 15-JUL-1999.

XX PP 29-DEC-1998; 98W0-CA01203.

PR 31-DEC-1997; 97US-0001737;
 XX PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 XX PT Mizzen L., Wisniewski J.;
 DR WPI: 1999-430397/36.

New nucleic acid encoding heat shock protein-60 from *Streptococcus*, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis.

PR Disclosure: Fig 10A-E, 17pp;
 XX English.

CC AA23905-30 represent heat shock proteins (Hsps). The specification describes *Streptococcus* Hsps, designated Hsp60. These proteins, their fragments, variants and fusion proteins, are used to elicit or enhance an immune response against *streptococcus*, and to elicit a similar response to target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. Also, where used for cancer control, they lack the side effects associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma, or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting *streptococci* in standard hybridization/amplification assays, and therapeutically in gene therapy vectors.

XX

Db	537	GFM	539	
RESULT 13				
ID	ABP39860	standard; Protein;	540 AA.	
XX				
AC	ABP39860;			
DR	24-JUL-2002	(first entry)		
DE	Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4705.			
XX	staphylococcus epidermidis: open reading frame; ORF; bacterial infection;			
KW	antibacterial; gene therapy.			
XX				
OS	Staphylococcus epidermidis.			
PN	US20030380370-B1.			
XX				
PD	30-APR-2002.			
XX				
PP	98US-0134001.			
XX				
PR	14-AUG-1997;	97US-055779P.		
XX				
PR	08-NOV-1997;	97US-06494P.		
XX				
PA	(GENO-) GENOME THERAPEUTICS CORP.			
XX				
PT	Doucelette-Stamm L.A., Bush D;			
XX				
DR	N-P5DB; ABN92405.			
XX				
PT	Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections - disclosure; SEQ ID 4705; 267pp; English.			
XX				
CC	ABM90538 to ABM93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP3124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for components able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.			
CC	N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.			
XX				
SQ	Sequence 540 AA;			
Query Match	68.9%; Score: 1833.5; DB: 23; Length: 540;			
Best Local Similarity	66.5%; Pred. No. 2_4e-110;			
Matches	359; Conservative: 87; Mismatches: 93; Indels: 1; Gaps: 1;			
OY	1 MAKEITKSADARAWMVRGVDMALDTKVITGPKRNVLKAFGSPLTNDGVTAKETE 60 II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II: 2 MAKDKJFSKEDARQAMIGRVDKLANAVVUTGPKRNVLKDFYTTPLNTDGVTAKETE 61 II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II: 3 LEDHFNMGAKLYEVSKNDAGDGTTTVAJQTAVHGLKVNAGANPIGRERIE 120 II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II: 62 LEDPYNMGAKLQEVANKNETAGDTTATVAQSMIQGKLKVTSGANPVLGRID 121 II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II: 121 TATAPEAKLIAQVSEKAIAQAVAVSRKVERVYTEAMRVENDVYITEE 180 II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II: 122 KAVOYAEHLTSOKVVKNEIAQVGAISADEBIGNYISEAMOKVENDGVITIE 181 II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II: 181 METELEVVGEGMDFDRYLSQYMTDNEMKADLNPFLTDKKSNTDIPLEBEVK 240 II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II: 182 PNTLEVEVGEGMDFDRYLSQYMTDNEMKADLNPFLTDKKSNTDIPLEBEVK 241 II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:II:			
PT	New nucleic acid encoding heat shock protein-60 from Streptococcus, useful in vaccines, as carriers for other immunogens, as anticancer agents and for diagnosis			
PT	disclosure; FIG 10A-B; 176pp; English.			
XX				
PS				
XX				
CC	AAV23905-30 represent heat shock proteins (Hsps). The specification, describes Streptococcal Hsps, designated Hsp60. These proteins, their fragments, variants and fusion proteins, are used to elicit or enhance an immune response against Streptococcus, and to elicit a similar response to a target antigen fused to the protein. Unlike other immunological carriers, Hsp60 proteins are not immunosuppressive so provide an increased response to any conjugated or fused antigen. As where used for cancer control, they lack the side effect associated with endotoxins. They can also be used to detect specific antibodies and in treatment or prevention of tumours (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or liver). The Hsp60 polynucleotide is used for recombinant production of the protein, as a source of primers and probes for detecting streptococci in standard hybridization/amplification assays, and therapeutically in gene therapy vectors.			

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Page 12

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